Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (CANCELED)

2. (CANCELED)

3. (CANCELED)

4. (CANCELED)

5. (CANCELED)

6. (CANCELED)

7. (CANCELED)

8. (CANCELED)

9. (CANCELED)

10. (CANCELED)

11. (CANCELED)

12. (PREVIOUSLY PRESENTED) A method of using a mutation scanning array to identify mutation in a target DNA sequence, wherein said mutation scanning array comprises a plurality of elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 5 different genes, wherein said method comprises:

(a) hybridizing the target DNA sequence with a control DNA sequence wherein said control DNA sequence is the wild-type DNA sequence corresponding to the target DNA sequence to create a duplex, and wherein said target DNA comprises a pool of nucleotide segments that collectively span at least 5 different genes;

(b) digesting the duplex to fragments of 50-300 base pairs, with restriction enzymes that allow generic addition of PCR primers;

(c) adding PCR primers to the duplex

(d) treating the duplex to remove any spontaneous aldehydes;

(e) reacting the duplex with a repair glycosylase to convert any mismatched sites in the duplex to reactive sites containing an aldehyde-containing abasic site;

(f) reacting the duplex with a compound of the formula X-Z-Y, wherein X is a detectable moiety, Y is NHNH2, O-NH2 or NH2, and Z is a hydrocarbon, alkyhydroxy, alkylethoxy, alkylester, alkylether, alkylamide or alkylamine, wherein Z may be substituted or unsubstituted; or where Z may contain a cleavable group; for a sufficient time and under conditions to covalently bind to the reactive sites;

(g) detecting the bound compound to identify sites of mismatches;

(h) isolating the DNA that contains mismatches from DNA without mismatches;

(i) PCR-amplifying the mismatch-containing DNA

(j) applying the mismatch-containing DNA on the Mutation Scanning Array, to determine the genomic position(s) where mismatches occur; and

k) determining whether the mismatch is a mutation or polymorphism.

13. (ORIGINAL) The method of claim 12, where the detectable moiety is selected from the group consisting of NH_2, SH, $NHNH_2$, a fluorescein derivative, a hydroxycoumarin derivative, a rhodamine derivative, a BODIPY derivative, a digoxigenin derivative and a biotin derivative.

14. (CANCELED)

15. (CANCELED)

16. (CURRENTLY AMENDED) The method of claim 12, wherein the target DNA sequence comprises at least 5 genes, wherein each individual whole gene is represented by a set of oligonucleotides which collectively spans that individual whole gene from the 5' to 3' end ~~each of which is contiguous~~.

17. (PREVIOUSLY PRESENTED) The method of claim 12, wherein the segments tagged with the detectable moiety are amplified before being used on the mutation scanning array.

18. (CURRENTLY AMENDED) The method of claim 12, wherein each ~~whole~~ gene on the mutation scanning array is represented by array elements; each element containing immobilized oligonucleotides that sample in 25-300 bases for the whole 3' to 5' mRNA sequence of each represented gene.

19. (PREVIOUSLY PRESENTED) The method of claim 12, wherein each of the array genes is represented by the coding portion of the gene.

20. (PREVIOUSLY PRESENTED) The method of claim 12, wherein each of the array genes is represented by both the coding and non-coding genomic portions of a gene.

21. (CURRENTLY AMENDED) The method of claim 12, wherein said at least 5 ~~at least 10~~ different array genes are collectively known to predispose an individual to a particular disease.

22. (PREVIOUSLY PRESENTED) The method of claim 21, where the disease is a particular kind of cancer.

23. (PREVIOUSLY PRESENTED) The method of claim 21, where the disease is a cardiovascular abnormality, or a neurodegenerative disorder, or diabetes.

24. (PREVIOUSLY PRESENTED) The method of claim 22, where said array genes are all known tumor suppressor genes or oncogenes.

25. (PREVIOUSLY PRESENTED) The method of claim 12, where said array genes are genes known to be overexpressed in a malignant cell, wherein overexpression is determined by comparison to the gene's expression in a corresponding non-malignant cell.

26. (NEW) A method of using a mutation scanning array to identify mutation in a target DNA sequence, wherein said mutation scanning array comprises a plurality of elements, wherein the elements contain immobilized oligonucleotides 8 - 50 bases long, that collectively span at least 5 different genes, wherein said method comprises:

(a) hybridizing the target DNA sequence with a control DNA sequence wherein said control DNA sequence is the wild-type DNA sequence corresponding to the target DNA sequence to create a duplex, wherein mismatches between said control DNA sequence and said target DNA correspond to positions of mutations or polymorphisms, and wherein said target DNA comprises a pool of nucleotide segments that collectively span at least 5 different genes;

(b) digesting the duplex to fragments of 50-300 base pairs, with restriction enzymes that allow generic addition of PCR primers;

(c) adding PCR primers to the duplex

(d) chemically modifying sites of mismatches in the target DNA in the duplex;

(e) covalently binding a ligand molecule to the chemically modified sites of mismatches;

(f) detecting the bound compound to identify sites of mismatches;

(g) isolating the DNA that contains mismatches from DNA without mismatches;

(h) PCR-amplifying the mismatch-containing DNA

(i) applying the mismatch-containing DNA on the mutation scanning array, to determine the genomic position(s) where mismatches occur; and

k) determining whether the mismatch is a mutation or polymorphism.